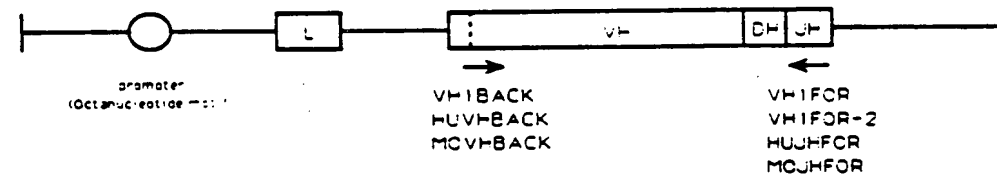
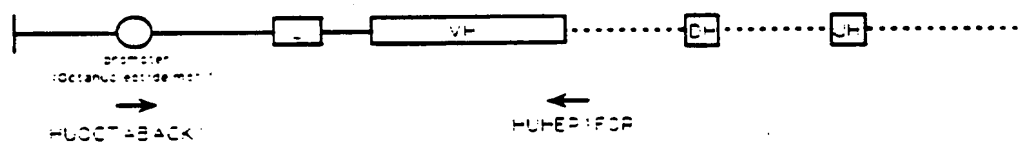


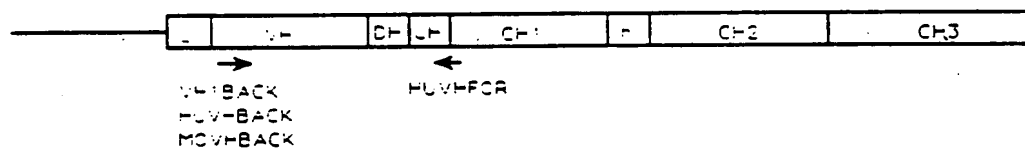
Rearranged heavy chain variable gene (DNA)



Unrearranged heavy chain variable gene (DNA)



Rearranged heavy chain variable gene (mRNA)



Rearranged light chain variable gene (DNA)

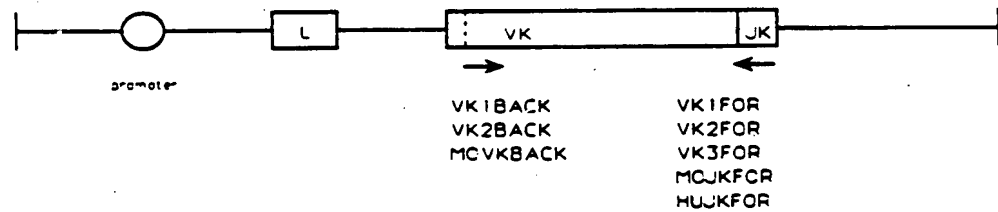


FIG. 1

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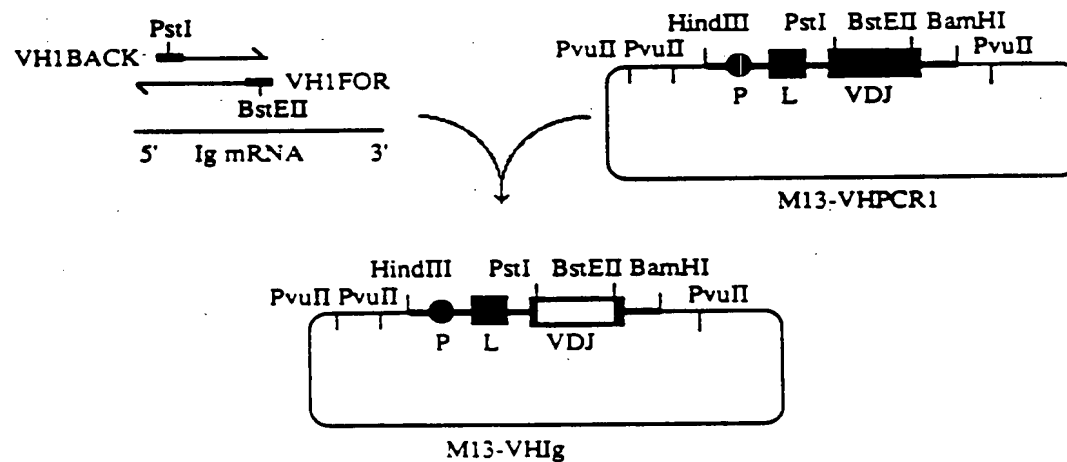


FIG. 2

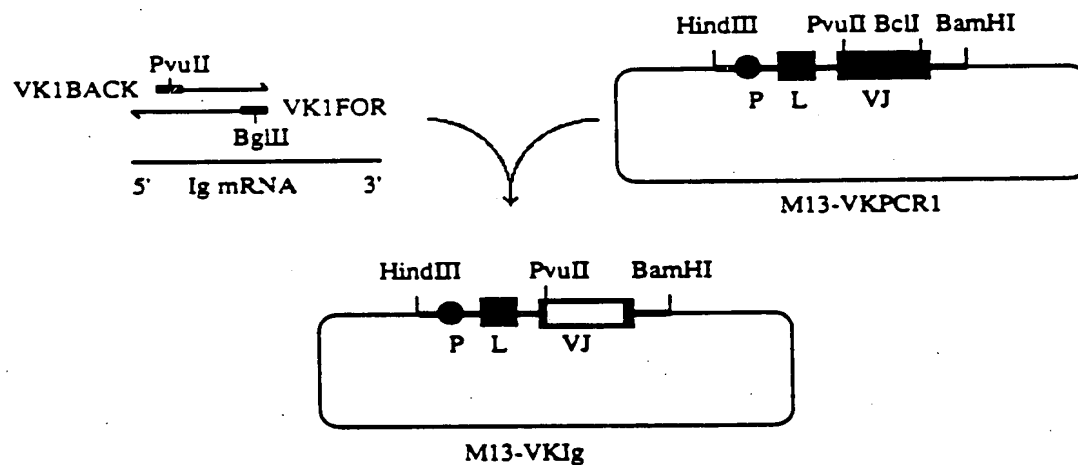


FIG. 4

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M13 VHPCR1

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Hind III

1
AAGCTTATGAATATGCAAAATCTCTGAAATCTACATGGTAAATATAGGTTTGTCTATACCA
10 20 30 40 50 60

CAAACAGAAAAACATGAGATCAGATTCTCTGACAGTTACTGAGCACACAGGACCTCAC
70 80 90 100 110 120

M G W S C I I L F L V A T A T
CATGGGATGGAGCTGTATCATCTCTCTCTGGTAGCAACAGCTACAGGTAAGGGGCTCAC
130 140 150 160 170 180

AGTAGCAGGCTTGAGGTCTGGACATATATATGGGTGACAAATGACATCCACTTTGCCTTTC
190 200 210 220 230 240

PstI

1 51 10
G V H S Q V Q L Q E S G P G L V R P
TCTCCACAGGTGTCTCACTCTCCAGGTCACCTGAGGAGAGCGGTCCAGGTCTGTGAGAC
250 260 270 280 290 300

CDR1

15 20 25 30
S Q T L S L T C T V S G S T F S S Y W M
CTAGCCAGACCTTGAGCTCTGACCTGACCTGTCAGGCTGTCTGGCAGCACCTTCAGCAGCTACTGGA
310 320 330 340 350 360

CDR2

35 40 45 50
H W V R Q P P G R G L E W I G R I D P N
TGCCTGGGTGAGACAGCCACCTGGACAGGTCTTGAGTGGATTGGAAGGATTGATCCTA
370 380 390 400 410 420

55 60 65 70
S G G T K Y N E K F K S R V T M L V D T
ATAGTGGTGGTACTAATGAGAGTTCAAGAGCAGAGTGACAATGCTGGTAGACA
430 440 450 460 470 480

75 80 85 90
S K N Q F S L R L S S V T A A D T A V Y
CCAGCAAGAACCACTTCAGCTGAGATTCAGCAGCGTGACAGCCGCCGACACCGCGGTCT
490 500 510 520 530 540

CDR3

95 100 105 110
Y C A R Y D Y Y G S S Y F D Y W G Q G T
ATTATGTGCAAGATAGGATTACTACGGTAGTAGCTACTTTGACTACTGGGGCCCAAGGGA
550 560 570 580 590 600

BstEII

115 120
T V T V S S
CCACGGTACCTCTCTCTCAGGTGAGTCTTACAACCTCTCTCTTCTATTTCAGCTTAAAT
610 620 630 640 650 660

AGATTTTACTGCAATTTGTTGGGGGGGAAATGTGTGTATCTGAATTTTCAGGTTCATGAAGGA
670 680 690 700 710 720

CTAGGGACACCTTGGGAGTCAGAAAGGTCATTGGGAGCCCGGCTGATGCAGACAGACA
730 740 750 760 770 780

BamHI

TCTCAGCTCCAGACTTCATGGCCAGAGATTTATAG
790 800 810

FIG. 3

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Hand III

CAAACAGAAAAACATGAGATCACAGTTTCTCTACAGTTACTGAGCACACAGGACCTCAC
98 108 118 128 138 148

M G W S C I L L F L V A T A T
CATGGGAAGGAGCTGTATCAACCTCTCTGGTAGCAACAGCTACAGGTAAGGGGCTCAC
158 168 178 188 198 208

AGTAGCAGGCTTGAGGTCGGACATATATATGGGTGACAAATGACATCCACTTTGCCTTTTC
218 229 238 248 258 268

25. 22

G V H S D I L S 10
 TTTCCACAGTGTCCACTCCGACATCTCTTACCCAGAGCCCAAGCAGCCTTGAGCGCCA
 275 295 308 318 328

132

15 20 25 30
V G D R V T T C R A S G G N I H N Y L A
GCGTGGGTGACAGAGTGACACTGACCTGTGAGAGCCAGCGGTAACTCCACAACCTACCTGG
338 348 358 368 378 388

CDR2

35 40 45 50
W Y Q Q K P G K A P K L L I Y Y T T T C
CTTGGTACCACGACAGAAGCCAGGTAAGGCTCAAGGCTGCTGATCTACTACACCACCACCC
398 408 418 428 438 448

55 60 65 70
A C G G V P S R F S G S G T D F T F T
TGGCTGACGGTGTGCCAAGCAGATTTCAGCGGTAGCGGTACCGGACTTCACCTTCA
458 468 478 488 498 508

CDR3

75 80 85 90
I S S L Q P E D I A T Y Y C Q H F W S T
CCATCAGCAGCCTCCAGCCAGGACATCGCCACCTACTACTGCCAGCACTTCTGGAGTA
518 528 538 548 558 568

Bcl I (requires *dam*⁻ host)

95 100 105 108
 P R T F G G G T K V V I K R
 CCCCAGGGACGTTCGGCCAGGGACCAAGGTGGTGGATCAACGTGAGTAGAATTTAAACT
 578 588 598 608 618 628

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TTGCTTCCTCAGTTCGTTGG
618 648

FIG. 5

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Sequence of MB1 VH

Splice -1
↓ G V H S
AGGTGTCCACTCC

1 PstI 10 20
Q V Q L Q E S G T E L A S P G A S V T L
CAGGTCCCACTTCAGGAGTCAAGAACTGAGCTGGCGAGTCTCTGGGGCATCAGTGACACTG
VH1BACK SITE

30 CDR1 40
S C K A S G Y T F T D H I N W V K K R
TCCTGCAAGGGTCTGGCTACACATTTACTGACCATATTATAAATTGGGTAAAAAGAGG
52a 53 CDR2
P G Q G L E W I G R I Y P V S G V T N Y
CCTGGACAGGGGCTTGGAGTGGATTGGAAGGATTTATCCAGTAAGTGGTGTAACTAACTAC
60 CDR2 65 70
N K F M G K A T F S V D R S S N T V Y
AATCAAAAATTTCATGGGCAAGGCCACATTTCTGTAGACCGGTCTCTCAACACAGTGTAC
80 82A B C 83 90 CDR3
M V L N S L T S E D P A V Y Y C G R G F
ATGGTGTGAACATCTGACATCTGAGGACCGTCTGTCTATTACTGTGGAAGGGGCTT
103 BstEII Splice
D F D V W G Q G T T V T V S S
GATTTTGACTACTGGGGCAAGGGGACACGGTCACTCTCTCTCAGG.....
VH1FOR SITE

Sequence of MB1 VK

Splice -1
↓ G V H S
AGGTGTCCACTCC

1 PvuII 10 20
D I Q L T Q S P P S L T V S V G E R V T
GACATTCAGGCTTCAGGAGTCTCTCCATCCCTGACTGTGTCACTAGGAGAGAGGGTCACT
VK1BACK SITE

27A B C D E F CDR1
I S C K S N O N L L W S G N R R Y C L G
ATCAGTTGCAAAATCCCAATCAGAATCTTTATGGAGTGGAAACCGAAGGTACTGTTTGGGC
35 40 50 CDR2
W H Q W K P G Q T P T P L I T W T S D R
TGGCACCAGTGGAAACCAAGGGCAAACTCCTACACCGTTGATCACCTGGACATCTGATAGG
60 70
F S G V P D R F I G S G S V T D F T L T
TTCTCTGGAGTCCCTGATCGTTTCATAGGCAGTGGATCTGTGACAGATTTCCTCTGACC
80 90 CDR3
I S S V Q A E D V A V Y F C Q Q H L D L
ATCAGCAGTGTGCAGGCTGAAGATGTGGCAGTTTATTCTGTGACCAACATTTGGACCTT
95 100 BglII/BclI Splice
P Y T F G G G T K L E I K
CCGTACAGTTCGGAGGGGGGACCAAGCTGGAGATCAAACGTGAG
VK1FOR SITE

FIG. 6

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α -Lys 30

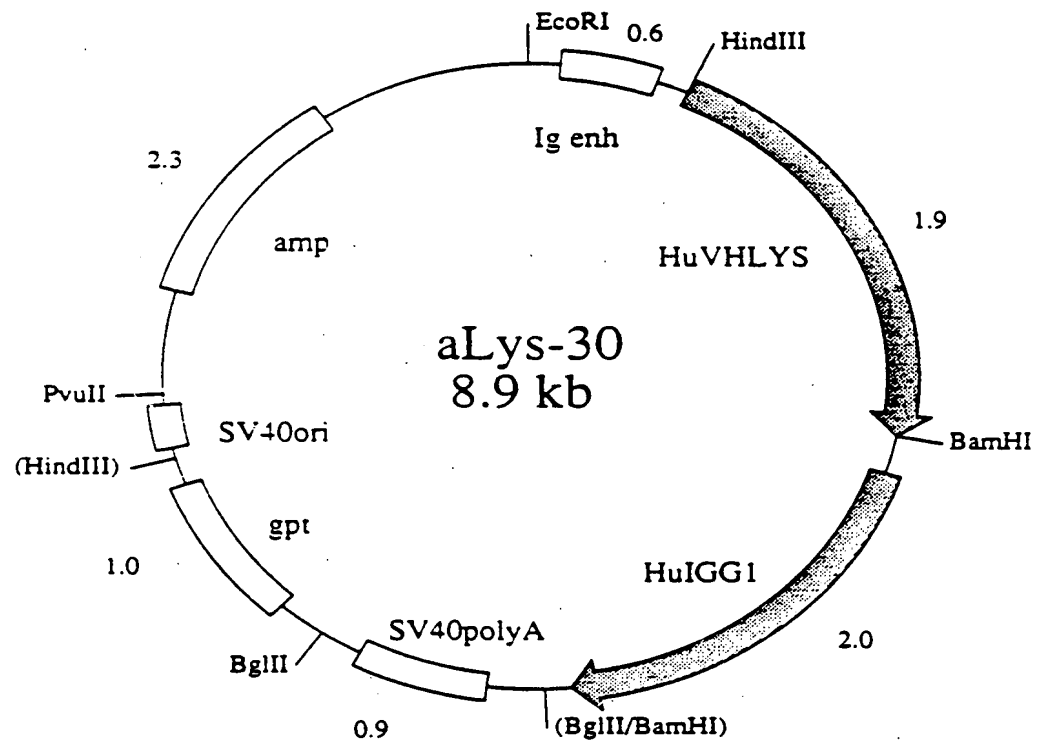


FIG. 7

α -Lys 17

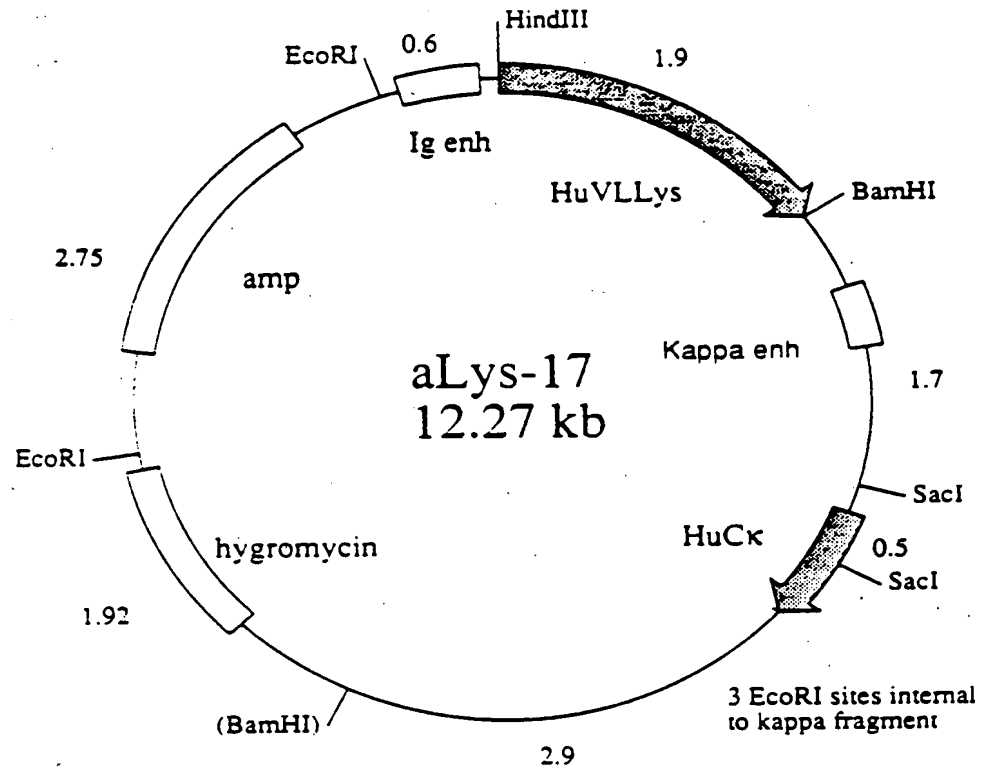


FIG. 8

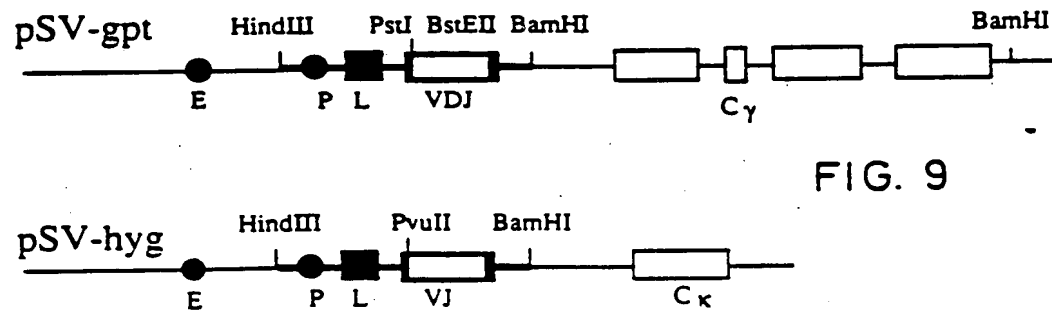


FIG. 9

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ER1

CDR1

ER2

CDR2

KABAT 1A

AC7	PGLVQPSQSLSTCTCSVTQYSIT	SGYWN	WRCPPGKLEWLG	YISYDGSNNYNPSLKN
AC9	PGLVQPSQSLSTCTCSVTQYSIT	SGYWN	WRCPPGKLEWLG	YISYDGSNNYNPSLKN
EC3	PGLVQPSQSLSTCTCSVTQYSIT	SGYWN	WRCPPGKLEWLG	YISYDGSNNYNPSLKN
GC1	PGLVQPSQSLSTCTCSVTQYSIT	SGYWN	WRCPPGKLEWLG	YISYDGSNNYNPSLKN

KABAT 1B

AC6	PVLVAPPSQSLSTCTCAVSDFSLT	SYGVH	WRCPPGKLEWLG	VHWAGGSTNYNSALMS
25G07	PGLVQPSQSLSTCTCTVSGFSLT	SYGVH	WRCPPGKLEWLG	VHWAGGSTDYNAAFIS
BC3	PGLVAPPSQSLSTCTCTVSGFSLT	SYGVH	WRCPPGKLEWLG	VHWAGGSTNYNSALMS
GC3	PGLVQPSQSLSTCTCTVSGFSLT	SYGVH	WRCPPGKLEWLG	VHWAGGSTDYNAAFIS
H09	PVLVAPPSQSLSTCTCTVSGFSLT	SYGVH	WRCPPGKLEWLG	VHWAGGSTNYNSALMS
25G10	PGLVAPPSQSLSTCTCTVSGFSLT	SYGVH	WRCPPGKLEWLG	VHWAGGSTNYNSALMS
AL2	PGLVAPPSQSLSTCTCTVSGFSLT	SYGVH	WRCPPGKLEWLG	VHWAGGSTNYNSALMS
AC8	PGLVAPPSQSLSTCTCTVSGFSLT	SYGVH	WRCPPGKLEWLG	VHWAGGSTNYNSALMS
25G08	PGLVAPPSQSLSTCTCTVSGFSLT	SYGVH	WRCPPGKLEWLG	VHWAGGSTNYNSALMS
AC3	PGLVQPSQSLSTCTCTVSGFSLT	SYGVH	WRCPPGKLEWLG	VHWAGGSTDYNAAFIS
CC7	PVLVAPPSQSLSTCTCTVSGFSLT	SYGVH	WRCPPGKLEWLG	VHWAGGSTNYNSALMS
H04	PGLVAPPSQSLSTCTCTVSGFSLT	SYGVH	WRCPPGKLEWLG	VHWAGGSTNYNSALMS

KABAT 11A

EC1	PELLVPPGVSXKLSCHKSGYTFE	DYAMH	WVQSPGKLEWLG	VISTYVGSASYNQKFKD
H07	PELLVPPGVSXKLSCHKSGYTFE	DYAMH	WVQSPGKLEWLG	VISTYVGSASYNQKFKD

KABAT 11B

AC1	AEILVPPGASVXLSCHKSGYTFE	SYAMH	WVQSPGKLEWLG	EIDPSSDSTNYNQKFKG
BC4	AEILVPPGASVXMSCHKSGYTFE	SYAMH	WVQSPGKLEWLG	EIDPSSDSTNYNQKFKG
CC3	AEILVPPGASVXLSCHKSGYTFE	SYAMH	WVQSPGKLEWLG	EIDPSSDSTNYNQKFKG
CC9	AEILVPPGASVXLSCHKSGYTFE	SYAMH	WVQSPGKLEWLG	EIDPSSDSTNYNQKFKG
CC6	AEILVPPGASVXMSCHKSGYTFE	SYAMH	WVQSPGKLEWLG	EIDPSSDSTNYNQKFKG
CC8	AEILVPPGASVXLSCHKSGYTFE	SYAMH	WVQSPGKLEWLG	EIDPSSDSTNYNQKFKG
EC7	AEILVPPGASVXLSCHKSGYTFE	SYAMH	WVQSPGKLEWLG	EIDPSSDSTNYNQKFKG
GC8	AEILVPPGASVXLSCHKSGYTFE	SYAMH	WVQSPGKLEWLG	EIDPSSDSTNYNQKFKG
GC10	AEILVPPGASVXLSCHKSGYTFE	SYAMH	WVQSPGKLEWLG	EIDPSSDSTNYNQKFKG
25G09	AEILVPPGASVXMSCHKSGYTFE	SYAMH	WVQSPGKLEWLG	EIDPSSDSTNYNQKFKG
FC4	AEILVPPGASVXLSCHKSGYTFE	SYAMH	WVQSPGKLEWLG	EIDPSSDSTNYNQKFKG
H04	AEILVPPGASVXLSCHKSGYTFE	SYAMH	WVQSPGKLEWLG	EIDPSSDSTNYNQKFKG
H01	AEILVPPGASVXLSCHKSGYTFE	SYAMH	WVQSPGKLEWLG	EIDPSSDSTNYNQKFKG
25G05	AEILVPPGASVXMSCHKSGYTFE	SYAMH	WVQSPGKLEWLG	EIDPSSDSTNYNQKFKG
BC1	AEILVPPGASVXMSCHKSGYTFE	SYAMH	WVQSPGKLEWLG	EIDPSSDSTNYNQKFKG
BC3	AEILVPPGASVXMSCHKSGYTFE	SYAMH	WVQSPGKLEWLG	EIDPSSDSTNYNQKFKG
BC1	AEILVPPGASVXMSCHKSGYTFE	SYAMH	WVQSPGKLEWLG	EIDPSSDSTNYNQKFKG

KABAT 111 A

25G03	GGLVQPGGSLSLSCAASGTFTE	DYVMS	WVQSPGKLEWLG	FIRNKANGYTTEYSASVKG
CC1	GGLVQPGGSLSLSCAASGTFTE	DYVMS	WVQSPGKLEWLG	FIRNKANGYTTEYSASVKG
BC7	GGLVQPGGSLSLSCAASGTFTE	DYVMS	WVQSPGKLEWLG	FIRNKANGYTTEYSASVKG

KABAT 111 B

GC5	GGLVQPGGSLSLSCAASGTFTE	DYVMS	WVQSPGKLEWLG	YISSGSGSTYYADTVKG
BC2	GGLVQPGGSLSLSCAASGTFTE	DYVMS	WVQSPGKLEWLG	YISSGSGSTYYADTVKG
CC4	GGLVQPGGSLSLSCAASGTFTE	DYVMS	WVQSPGKLEWLG	YISSGSGSTYYADTVKG
CC3	GGLVQPGGSLSLSCAASGTFTE	DYVMS	WVQSPGKLEWLG	YISSGSGSTYYADTVKG
FC2	GGLVQPGGSLSLSCAASGTFTE	DYVMS	WVQSPGKLEWLG	YISSGSGSTYYADTVKG
FC6	GGLVQPGGSLSLSCAASGTFTE	DYVMS	WVQSPGKLEWLG	YISSGSGSTYYADTVKG
CC2	GGLVQPGGSLSLSCAASGTFTE	DYVMS	WVQSPGKLEWLG	YISSGSGSTYYADTVKG
FC9	GGLVQPGGSLSLSCAASGTFTE	DYVMS	WVQSPGKLEWLG	YISSGSGSTYYADTVKG

KABAT 111 C

EC6	GGLVQPGGSLSLSCAASGTFTE	DYVMS	WVQSPGKLEWLG	FIRNKANGYTTEYSASVKG
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KABAT V A

CC4	AEILVPPGASVXLSCHKSGYTFE	SYAMH	WVQSPGKLEWLG	EIDPSSDSTNYNQKFKG
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FIG. 10a

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CDR 2

FRAMTWORK 3

CDR 3

KABAT HUMAN VH1

	STSTAYMELSLRSED TAVYYCAR	GEGWQHFDY
HACKFQG	RVTIRRHKSTSTAYMELSSLRSED TAVYYCAR	GSRYGYDCSGYYL
GYACKFQG	RVTMTNTSISTATMELSSLRSED TAVYYCAR	LAHFGSPVDWFD

KABAT HUMAN VH2

KHQLQPSLKS	RVTISVDTSKNQFSLKLSVTAAD TAVYYCAR	GGVVPAAIMDV
KS	RVTISVDTSKNQFSLKLSVTAAD TAVYYCAR	MARYYDFWSGYSAYYDY
SLKS	RLSISGQTSRNQFSLKLSVTAAD TAVYYCAR	HRNWGSPVHFQY
	ESTSTAYMELSSLRSED TAVYYCAR	DSYGQYGGHY

KABAT HUMAN VH3

ISYITSSSSYTNVADSVKG	RFTISRDNAKNSLYLQMNSLRAED TAVYYCAR	DGRFGTYSPSDY
SVKG	RFTISRDDSKSIAYLQVNSLKTED TAVYYCTR	TIYYDSSGYPYW
YADSVKG	RFTISRDNAKNSLYLQMNSLRAED TAVYYCAR	GIALDAFDI
YYADSVRO	RFTISRDNKNTLYLQMNSLRAED TAVYYCAR	53 NT. UNPROD REARR
DSVKG	RFTISRDNAKNSLYLQMNSLRDEED TAVYYCAR	DHSGTGCGGSGSYF
VSAISGSGGSTYYADSVKG	RFTISRDNKNTLYLQMNSLRSED TAVYYCAR	KDNLWFDP
AVISYDGSNKYYADSVKG	RFTISRDNKNTLYLQMNSLRAED TAVYYCAR	DLGGRGVVVVPAPGGRSIIYYGMDV
GAVISYDGSNKYYADSVKG	RFTISRDNKNTLYLQMNSLRAED TAVYYCAR	LEGIGTIYYYGMDV
	AKNSLYLQMNSLRAED TAVYYCVR	DDSSSWPKHFQ
QYAASVKG	RFTISRDDSKNSLYLQMNSLNTED TAVYYCVR	SGVVPYLDY

KNOWN FAMILY

AVYYCAR	DPRIAARPDYYYYMDV
TAMYYCAR	GAEVVEPTARYYYGLNV

FIG. 11

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FR1	CDR1	FR2
YTTT	SYGIS	WVTTGPWTRCLRWMG
GEKPGSSVKV/SCKASGYTFT	DYFMN	WMRQAPGQRLWWMG
QVQLQEIIGPRTGEASETSLSLICAVSGDSIS	SGNW*1	WVRQPPGKGLEWIG
QVQLQESGPGGLVK*SETLSLTCTVSGGSIS	SYIWS	WIRQPPGKGLEWIG
GYTFT	NYCMH	WVRQDHAQGLEWIM
QVQLQESGPGGLVKpSETLSLYCAVSGDSIS	SGNW*1	WVRQPPGKGLEWIG
GPRLGEASETSLSLTCTVSGGSIS	SSSYW	WIRQPPGKGLEWIG
QVQLQESGPGGLVKpSETLSLTCTVSGGSIS	SYIWS	WIRQPPGKGLEWIG
LSLICAVSGGSIS	SGNW*1	WVRQPPGKGLEWIG
SETLSLTCAVYGGSF	GYIWS	WIRQPPGKGLEWIG
QVQLVQSGAEVKKPGASVKV/SCKASGYTFT	NYCMH	WVRQVLAQGLEWIM
SETLSLICAVSGDSIS	SGNW*1	WVRQPPGKGLEWIG
SRAQTGEASETSLSLTCTVSGGSIS	SSSYWG	WIRQPPGKGLEWIG
CPLTCTVSGGSVSSGS	YIWS	WIRQPPGKGLEWIG
GLVKPSETLSLTCTVSGGSIS	SYIWS	WIGSPGKGLEWIG
SFETLSLICAVSGDSIS	SGNW*1	WVRQPPGKGLEWIG
QVQLVQSGAEVKKPGSSVKV/SCKASGDTT	SYAIS	WVRQAPGQGLEWIM
QVQLQGWGAGLLKPSSETLSLTCAVYGGSF	GYIWS	WIRQPPGKGLEWIG
QVQLQESGPGGLVKpSETLSLTCTVSGGSIS	SSSYWG	WIRQPPGKGLEWIG
GPGLVKPSQTLSTCTVSGGSIS	SGGYWS	WIRQNP G K G L E W I G

* indicates stop codon (unsure as sequence remains in frame)
• sequence terminates due to internal restriction site
lower case denotes frame shift

CDR1	FR2	CDR3
WISAYNGNTNYAQKLCG	RVTITDTSSTAYMELSLRSDDTAVYYCAR	DTVSS
WINAGNGNTKYSQKLCG	RVTITRDTASTAYMQLSSLRSED TAVYYCAR	DTVSS
EIHHS GSTYYP SLKS	RITMSVDT SKNQ FYLKLSS	
RIYTS GSTYYP SLKS	RVTISVDT SKNQ FSLKLSSVTAADTAVYYCAR	DTVSS
LVCPSD GSTSYAQKFQA	RVTITRDTSMSTAYMELSSLRSED TAVYYCAR	DTVSS
EIHHS GSTYYP SLKS	RITMSVDT SKNQ FYLKLSS	
EIHHS GSTYYP SLKS	RVTISVDT SKNQ FSLKLSS	
YIYYS GSTYYP SLKS	RVTISVDT SKNQ FSLKLSS	
EIHHS GSTYYP SLKS	RITMSVDT SKNQ FYLKLSS	
EIHHS GSTYYP SLKS	RVTISVDT SKNQ FSLKLSSVTAADTAVYYCAR	DTVSS
LVCPSD GSTSYAQKFQA	RVTITRDTSMSTAYMELSSLRSED TAVYYCAR	DTVSS
EIHHS GSTYYP SLKS	RITMSVDT SKNQ FYLKLSS	
SIYYS GSTYYP SLKS	RVTIPVDT SKNQ FSLKLSS	
YIYYS GSTYYP SLKS	RVTISVDT SKNQ FSLKLSSVTAADTAVYYCAR	DTVSS
RIYTS GSTYYP SLKS	RVTMSVDT SKNQ FSLKLSS	
EIHHS GSTYYP SLKS	RITMSVDT SKNQ FYLKLSS	
RIIPILGIAN YAQKFQG	RVTITADKSTAYMELSSLRSED TAVYYCAR	DTVS
EIHHS GSTYYP SLKS	RVTISVDT SKNQ FSLKLSS	
EIHHS GSTYYP SLKS	RVTISVDT SKNQ FSLKLSS	
YIYYS GSTYYP SLKS	RVTISVDT SKNQ FSLKLSSVTAADTAVYYCAR	DTVSS

FIG. 12

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psw.

HindIII site AAGCTT

GCATSCAAATTTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCTACGGCAGCC
10 20 30 40 50 60

M K Y L L P T A A
A S L L L L A A Q P A M A Q V Q L Q E S
GCTGGATTGTTTATTACTCGCTGCCCCAACCAGCGATGGCCCAGGTGCAGGTGCAGGAGTCA
70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
GGACCTGGCTTGGTGGCTGGCTGACAGAGCGTGTCCATCAGTGCACCGTCTCAGGGTTC
130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
TCATTAACCGGCTATGGTGTAAACTGGGTTCGCCAGCGCTCCAGGAAAGGCTCTGGAGTGG
190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTTGGGGTGTATGGAACACAGACTATAATTGAGCTCTCAAATCCAGACTG
250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAACTCCAAAGAGCCAAAGTTTCTTAAAAATGAACAGTCTGCACACT
310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATTATAGGCTTGACTACTGGGGC
370 380 390 400 410 420

Q G T T V T V S S SmaI
CAAGGCACCACGGTCACCGTCTCTCATAATAAGAGCTATCGGGGCTAAGCTCGAATTC
430 440 450 460 470 480

FIG. 13

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PSW2

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HindIII AAGCTT

GCATGCAAAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCGCTACGGCAGCC
10 20 30 40 50 60

AGLLLLAQAQPMQAQVQLQES
GCTGGATTGTTATTACTCGCTGCGCAACAGCGATGGCCAGGTGCAGCTGCAGGAGTCA
70 80 90 100 110 120

GPGLVAPSSQLSITCTVSGF
GGACCTGGCCCTGGTGGCGCCCTCACAGCGCTGTCCATCACATGCACCGTCTCAGGGTTC
130 140 150 160 170 180

SLTG YGVNWVRQP PGKGLEW
TCATTAAACCGGCTATGGTGTAAACTGGGTTGCGCAACCTCCAGGAAAGGGTCTGGAGTGG
190 200 210 220 230 240

LGM I WGDGNTDYN SALKSRL
CTGGGAATGATTTGGGGTGATGGAACACAGACTATAATTCAGCTCTCAAATCCAGACTG
250 260 270 280 290 300

SISKDN S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAACTCCCAAGAGCCCAAGTTTCTTAAAAATGAACAGTCTGCACACT
310 320 330 340 350 360

DDTARYYCARERDYRLDYWG
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATTATAGGCTTGACTACTGGGGC
370 380 390 400 410 420

QGT TVTVSS
CAAGGCACCAAGGCTCAGCTGTCTCTCATAATAAGAGCTCGAATTCGCCAAGCTTGCATGC
430 440 450 460 470 480

AAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCGCTACGGCAGCGCTGGA
490 500 510 520 530 540

LLLLAQAQPMADIVLTQSPA
TTGTTATTACTCGCTGCGCAACAGCGATGGCCGACATCGTCTGACTCAGTCTCCAGCC
550 560 570 580 590 600

SLSA SVGETVTITCRASGNI
TCCCTTTCTGCGTCTGTGGGAGAACTGTCCCATCACATGTGAGCAAGTGGGAATATT
610 620 630 640 650 660

HNYLAWYQKQGKSPQLLVY
CACAATTATTTAGCATGGTATTCAGCAGAAACAGGAAAAATCTCTCAGCTCTCTGGTCTAT
670 680 690 700 710 720

FIG. 14a

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Y T T T L A D G V P S R F S G S G S G T
TATACAACAACCTTAGCAGATGGTGTGCCATCAAGGTTGAGTGGCAGTGGATCAGGAACA
730 740 750 760 770 780

Q Y S L K I N S L Q P E D F G S Y Y C Q
CAATATTCTCTCAAGATCAACAGCGCTGCAACCTGAAGATTTTGGGAGTTATTACTGTCAA
790 800 810 820 830 840

H F W S T P R T F G G G T K L E I K R
CATTTTGGAGTACTCCTCGGACGTTGCGTGGAGGCACCAAGCTGGAAATCAAACGGTAA
850 860 870 880 890 900

TAAGAGCTCGAATTC
910

FIG. 14 b

pSWLHPOLYMYC

HindIII site AAGCTT

M K Y L L P T A A
GCATGCAAAATTCATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q
GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCCAGGTGCAGCTGCAG
70 80 90 100 110 PstI

Polylinker

TCTAGA GTCGAC CTCGAG
XbaI SalI XhoI

MYC PEPTIDE

V T V S S E O K L I S E E D L N * *
GGTCACCGTCTCCTCAGAACAAAACTCATCTCAGAAGAGGATCTGAATTAATAA
BstEII

GGGCTAAGCTCGAATTC

FIG. 15

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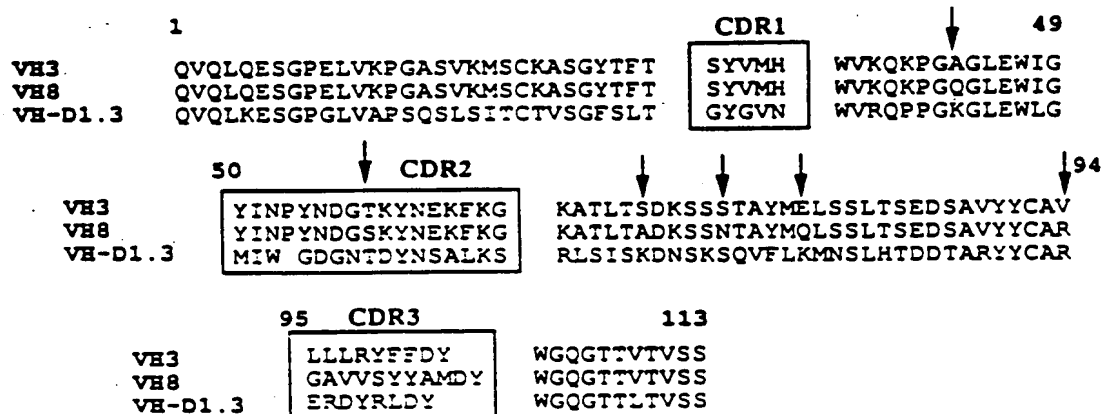


FIG. 16

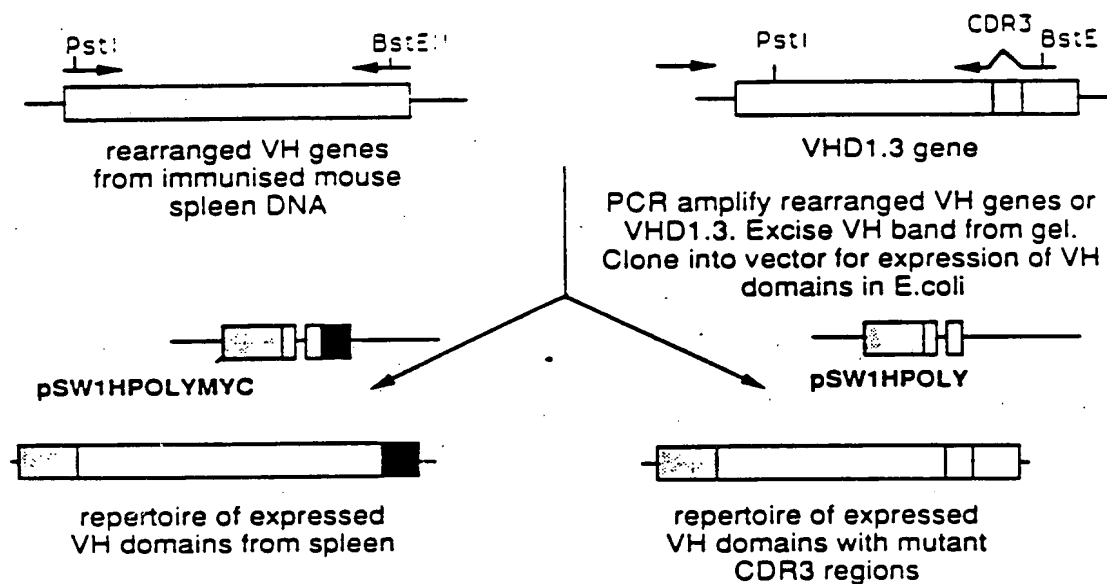
FR1	QVQLQESGGGLVQPGGSLRLSCAASGFTFS	
	SYAMS	CDR1
FR2	WVRQAPGKGLEWVS	
	AISGSGGSTYYADSVKG	CDR2
FR3	RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAM	
	WRGIATPVSF⁹⁴DLGYFDY	CDR3

FIG. 17

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Assay for binding to antigen

FIG. 18

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PSW2HPCLY

HindIII AAGCTT

GCATGCAAAATTCATTTCAAGGAGACAGTCATAATGAAATACCTATTGCGCTACGGCAGCC
10 20 30 40 50 60

AGLLLLAQAQVQLQ
GCTGGATTGTTATTACTGCGCTGCCCAACCAGCGATGGCCAGGTGCAGCTGCAG
70 80 90 100 110 PstI

TCTAGA GTCGAC CTCGAG
XbaI SalI XhoI

VTVS
GGTCACCGTCTCTCATAATAAGAGCTCGAATTCGCCAAGCTTGCATGC
EcoRII 430 440 450 460 470 480

MAKYLPLTAAAG
AAATTCATTTCAAGGAGACAGTCATAATGAAATACCTATTGCGCTACGGCAGCGCTGGA
490 500 510 520 530 540

LLLLAQAQADIVLTQSPA
TTGTTATTACTGCGCTGCCCAACCAGCGATGGCCAGCATCGTCTGACTCAGTCTCCAGCC
550 560 570 580 590 600

SLSA SVGETVTITCRASGN I
TCCCTTTCTGCGCTCTGTGGGAGAAACTGTCCACCATCAGTCTGAGCAAGTGGGAATATT
610 620 630 640 650 660

HN YLAWYQQKQGKSPQLLVY
CACCAATTATTAGCATGGTATCAGCAGAAACAGGGAAATCTCTCAGCTCCTGGTCTAT
670 680 690 700 710 720

YTTLADGVPSRFSGSGSGT
TATACAACAACCTTAGCAGATGGTGTGCCATCAAGGTTCAAGTGGCAGTGGATCAGGAACA
730 740 750 760 770 780

QYSLKINSLOPEDFGSY YCQ
CAATATTCTCTCAAGATCAACAGCGCTGCAACCTGAAGATTTGGGAGTTATTACTGTCAA
790 800 810 820 830 840

HFWSTPRTFGGGTKLEIKR
CATTTTGGAGTACTCTCGGACGTTGCGGTGGAGGCACCAAGCTGGAATCAAACGGTAA
850 860 870 880 890 900

TAAGAGCTCGAATTC
910

FIG. 19

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M K Y L L P T

AAGCTTGCATGCAAATTCATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACG
10 20 30 40 50 60

A A A G L L L L A A Q P A M A Q V Q L Q
GCAGCCGCTGGATTGTTTACTCGCTGCCCAACCAGCGATGGCCCGAGGTGCAGCTGCAG
70 80 90 100 110 120

E S G P G L V A P S Q S L S I T C T V S
GAGTCAGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCA
130 140 150 160 170 180

G F S L T G Y G V N W V R Q P P G K G L
GGGTTCTCATTAAACCGCTATGGTGTAAACTGGGTTGCCAGCCTCCAGGAAAGGGTCTG
190 200 210 220 230 240

E W L G M I W G D G N T D Y N S A L K S
GAGTGGCTGGGAATGATTGGGGTGATGGAAACACAGACTATAATTAGCTCTCAAATCC
250 260 270 280 290 300

R L S I S K D N S K S Q V F L K M N S L
AGACTGACATCAGCAAGGACAACTCCAAGAGCCAGTTTCTTAAAAATGAACAGTCTG
310 320 330 340 350 360

H T D D T A R Y Y C A R E R D Y R L D Y
CACACTGATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATTATAGGCTTGACTAC
370 380 390 400 410 420

W G Q G T T V T V S S G G G A P A A A P
TGGGGCCCAAGGCACCAACGGTCAACGGTCTCTCAGGTGGTGGTGGTCCAGCAGCTGCACCT
430 440 450 460 470 480

A G S G C V Q L K E S G P G L V A P S Q
GCTGGAGGAGGACAGGTGCAGCTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCTCACAG
490 500 510 520 530 540

S L S I T C T V S G F S L T G Y G V N W
AGCCTGTCCATCACATGCACCGTCCAGGGTTCTCATTAAACCGGCTATGGTGTAAACTGG
550 560 570 580 590 600

V R Q P F G K G L E W L G M I W G D G N
GTTGCCAGCCTCCAGGAAAGGGTCTGGAGTGGCTGGGAATGATTGGGGTGATGGAAAC
610 620 630 640 650 660

T D Y N S A L K S R L S I S K D N S K S
ACAGACTATAATTAGCTCTCAAATCCAGACTGAGCATCAGCAAGGACAACTCCAAGAGC
670 680 690 700 710 720

Q V F L K M N S L H T D D T A R Y Y C A
CAAGTTTCTTAAAAATGAACAGTCTGCACACTGATGACACAGCCAGGTACTACTGTGCC
730 740 750 760 770 780

R E R D Y R L D Y W G Q G T T V T V S S
AGAGAGAGAGATTATAGGCTTGACTACTGGGGCCCAAGGCACCAACGGTCAACCGTCTCTCA
790 800 810 820 830 840

TAATAAGAGCTC
850

FIG. 20

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M K Y L L P T A A

GCATGCAAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
 10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q E S
 GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCAGGTGCAGCTGCAGGAGTCA
 70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
 GGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
 130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
 TCATTAACCGGCTATGGTGTAACTGGGTTGCCAGCCTCCAGGAAAGGGTCTGGAGTGG
 190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
 CTGGGAATGATTTGGGGTGATGGAACACAGACTATAATTCAGCTCTCAAAATCCAGACTG
 250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
 AGCATCAGCAAGGACAACTCCAGAGCCAGTTTTCTTAAAAATGAACAGTCTGCACACT
 310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
 GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATTATAGGCTTGACTACTGGGGC
 370 380 390 400 410 420

Q G T T V T V S S R T P E M P V L E N R
 CAAGGCACCCAGGTCACCGTCTCCTCACGGACACCAGAAATGCCTGTTCTGGAAAACCGG
 430 440 450 460 470 480

A A Q G D I T A P G G A R R L T G D Q T
 GCTGCTCAGGGCGATATTACTGCACCCGGCGGTGCTCGCCGTTTAAACGGGTGATCAGACT
 490 500 510 520 530 540

A A L R D S L S D K P A K N I I L L I G
 GCCGCTCTGCGTATTTCTTTAGCGATAAACCTGCAAAAAATATTATTTTGCTGATTGGC
 550 560 570 580 590 600

D G M G D S E I T A A R N Y A E G A G G
 GATGGGATGGGGGACTCGGAAATTACTGCCGCACGTAATTATGCCGAAGGTGCGGGCGGC
 610 620 630 640 650 660

F F K G I D A L P L T G Q Y T H Y A L N
 TTTTTAAAGGTATAGATGCCTTACCGCTTACCGGGCAATACACTCACTATGCGCTGAAT
 670 680 690 700 710 720

K K T G K P D Y V T D S A A S A T A W S
 AAAAAACCGGCAACCGGACTACGTACCGACTCGGCTGCATCAGCAACCGCTGGTCA
 730 740 750 760 770 780

FIG. 21a

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T G V K T Y N G A L G V D I H E K D H P
ACCGGTGTCAAAACCTATAACGGCGCGCTGGGCGTTCGATATTCACGAAAAAGATCACCCA
790 800 810 820 830 840

T I L E M A K A A G L A T G N V S T A E
ACGATTCTGGAAATGGCAAAAGCCGCGAGGTCTGGCGACCGGTAACGTTTCTACCGCAGAG
850 860 870 880 890 900

L Q D A T P A A L V A H V T S R K C Y G
TTGCAGGATGCCACGCCCGCTGCGCTGGTGGCACATGTGACCTCGCGCAAATGCTACGGT
910 920 930 940 950 960

P S A T S E K C P G N A L E K G G K G S
CCGAGCGCGACCAAGTGAATAATGTCCGGGTAAACGCTCTGGAAAAAGGCGGAAAGGATCG
970 980 990 1000 1010 1020

I T E Q L L N A R A D V T L G G G A K T
ATTACCGAACAGCTGTTAACGCTCGTGCCGACGTTACGCTTGGCGGCGGCGCAAAACC
1030 1040 1050 1060 1070 1080

F A E T A T A G E W Q G K T L R E Q A Q
TTTGCTGAAACGGCAACCGCTGGTGAATGGCAGGGAACGCTGCGTGAACAGGCACAG
1090 1100 1110 1120 1130 1140

A R G Y Q L V S D A A S L N S V T E A N
GCGCGTGGTTATCAGTTGGTGAGCGATGCTGCCTCACTGAATTCGGTGACGGAAGCGAAT
1150 1160 1170 1180 1190 1200

Q Q K P L L G L F A D G N M P V R W L G
CAGCAAAAACCCCTGCTTGGCCTGTTGCTGACGGCAATATGCCAGTGCGCTGGCTAGGA
1210 1220 1230 1240 1250 1260

P K A T Y H G N I D K P A V T C T P N P
CCGAAAGCAACGTACCATGGCAATATCGATAAGCCCGCAGTCACCTGTACGCCAAATCCG
1270 1280 1290 1300 1310 1320

Q R N D S V P T L A Q M T D K A I E L L
CAACGTAATGACAGTGATACCAACCCCTGGCGCAGATGACCGACAAAGCCATTGAATTGTTG
1330 1340 1350 1360 1370 1380

S K N E K G F F L Q V E G A S I D K Q D
AGTAAAAATGAGAAAGGCTTTTCTCTGCAAGTTGAAGGTGCGTCAATCGATAAACAGGAT
1390 1400 1410 1420 1430 1440

H A A N P C G Q I G E T V D L D E A V Q
CATGCTGCGAATCCTTGTGGGCAAATGGCGAGACGGTCGATCTCGATGAAGCCGTACAA
1450 1460 1470 1480 1490 1500

R A L E F A K K E G N T L V I V T A D H
CGGGCGCTGGAATTCGCTAAAAAGGAGGGTAACACGCTGGTCATAGTCACCGCTGATCAC
1510 1520 1530 1540 1550 1560

FIG. 21b

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A H A S Q I V A P D T K A P G L T Q A L
GCCCACGCCAGCCAGATTGTTGCCCGGATACCAAAGCTCCGGGCCTCACCAGGCGCTA
1570 1580 1590 1600 1610 1620

N T K D G A V M V M S Y G N S E E D S Q
AATACCAAAGATGGCGCAGTGATGGTGTGAGTTACGGGAACCTCCGAAGAGGATTACAA
1630 1640 1650 1660 1670 1680

E H T G S Q L R I A A Y G P H A A N V V
GAACATACCGGCAGTCAGTTGCGTATTGCCGCGTATGGCCCCGATGCCGCCAATGTTGTT
1690 1700 1710 1720 1730 1740

G L T D Q T D L F Y T M K A A L G L K *
GGACTGACCGACCGACCGATCTCTTCTACACCATGAAAGCCGCTCTGGGGCTGAAATAA
1750 1760 1770 1780 1790 1800

AACCGCGCCCGGAGTGAAATTTTCGCTGCCGGTGGTTTTTTTCTGTTAGC
1810 1820 1830 1840 1850

FIG. 21c

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GCATGCAAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
10 20 30 40 50 60

M K Y L L P T A A
A G L L L L A A Q P A M A Q V Q L Q E S
GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCCAGGTGCAGCTGCAGGAGTCA
70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
GGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
TCATTAAACCGGCTATGGTGTAACCTGGGTTTCGCCAGCCTCCAGGAAAGGTTCTGGAGTGG
190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTTGGGGTGATGGAAACACAGACTATAATTCAGCTCTCAAATCCAGACTG
250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAAGTCCAAGAGCCAAGTTTCTTAAAAATGAACAGTCTGCACACT
310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTACTGGGGC
370 380 390 400 410 420

Q G T T V T V S S * *
CAAGGCACCACGGTCACCGTCTCCTCATAATAAGAGCTATCCCGGGAGCTTGCATGCAAA
430 440 450 460 470 480

M K Y L L P T A A A G L
TTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTG
490 500 510 520 530 540

L L L A A Q P A M A D I E L V D L E I K
TTATTACTCGCTGCCCAACCAGCGATGGCCGACATCGAGCTCGTCGACCTCGAGATCAAA
550 560 570 580 590 600

R E Q K L I S E E D L N * *
CGGGAACAAAACCTCATCTCAGAAGAGGATCTGAATTAATAATGATCAAACGGTAATAAG
610 620 630 640 650 660

GATCCAGCTCGAATTC
670

FIG. 22

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Q V Q L Q E S G P G L V Q P S Q S L S I
 CAGGTGCAGCTGCAGGAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATC
 10 20 30 40 50 60
 T C T V S G F S L T S Y G V H W V R Q S
 ACCTGCACAGTCTCTGGTTTCTCATTAACTAGCTATGGTGTACACTGGGTTCCGCCAGTCT
 70 80 90 100 110 120
 P G K G L E W L G M I W G D G N T D Y N
 CCAGGAAAGGGTCTGGAGTGGCTGGGAATGATTGGGGTGATGGAAACACAGACTATAAT
 130 140 150 160 170 180
 S A L K S R L S I S K D N S K S Q V F L
 TCAGCTCTCAAATCCAGACTGAGCATCAGCAAGGACAACCTCCAAGAGCCAAGTTTCTTA
 190 200 210 220 230 240
 K M N S L H T D D T A R Y Y C A R E R D
 AAAATGAACAGTCTTGCACACTGATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGAT
 250 260 270 280 290 300
 Y R L D Y W G Q G T T V T V S S
 TATAGGCTTGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
 310 320 330 340

FIG. 23

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